

M. Wilson

1633

RAW SEQUENCE LISTING DATE: 06/21/2000  
PATENT APPLICATION: US/09/451,291 TIME: 10:52:34

Input Set : A:\Sequence  
Output Set: N:\CRF3\06212000\I451291.raw

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JUL 17 2000

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4 <110> APPLICANT: Chen, Lieping  
6 <120> TITLE OF INVENTION: B7-H1, A NOVEL IMMUNOREGULATORY MOLECULE  
8 <130> FILE REFERENCE: 07039/187001  
10 <140> CURRENT APPLICATION NUMBER: US 09/451,291  
11 <141> CURRENT FILING DATE: 1999-11-30  
13 <160> NUMBER OF SEQ ID NOS: 12  
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 290  
19 <212> TYPE: PRT  
20 <213> ORGANISM: Homo sapiens  
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23 Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu  
24 1 5 10 15  
25 Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr  
26 20 25 30  
27 Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu  
28 35 40 45  
29 Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile  
30 50 55 60  
31 Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser  
32 65 70 75 80  
33 Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn  
34 85 90 95  
35 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr  
36 100 105 110  
37 Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val  
38 115 120 125  
39 Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val  
40 130 135 140  
41 Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr  
42 145 150 155 160  
43 Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser  
44 165 170 175  
45 Gly Lys Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn  
46 180 185 190  
47 Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr  
48 195 200 205  
49 Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu  
50 210 215 220  
51 Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His  
52 225 230 235 240  
53 Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr  
54 245 250 255  
55 Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys  
56 260 265 270  
57 Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu

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58          275          280          285
59 Glu Thr
60      290
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 870
63 <212> TYPE: DNA
64 <213> ORGANISM: Homo sapiens
65 <400> SEQUENCE: 2
68 atgaggatat ttgctgtctt tatattcatg acctactggc atttgcgtgaa cgcatttact      60
69 gtcacggttc ccaaggacct atatgtggtg gagtatggta gcaatatgac aattgaatgc      120
70 aaattcccgag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag      180
71 gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaagggtca gcatagtagc      240
72 tacagacaga gggcccggtc gttgaaggac cagctctccc tgggaaatgc tgcacttcag      300
73 atcacagatg tgaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt      360
74 gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga      420
75 atttgggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac      480
76 cccaaggccg aagtcactcg gacaagcagt gaccatcaag tcctgagtgg taagaccacc      540
77 accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac      600
78 acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaccat      660
79 acagctgaat tggatcatcc agaactacac ctggcacatc ctccaaatga aaggactcac      720
80 ttggtaatte tggagaccat cttattatgc cttggtgtag cactgacatt catcttccgt      780
81 ttaagaaaag ggagaatgat ggaatgtgaaa aaatgtggca tccaagatag aaactcaaa      840
82 aagcaaaagt atacacattt ggaggagacg
83 <210> SEQ ID NO: 3
84 <211> LENGTH: 290
85 <212> TYPE: PRT
86 <213> ORGANISM: Mus musculus
87 <400> SEQUENCE: 3
90 Met Arg Ile Phe Ala Gly Ile Ile Phe Thr Ala Cys Cys His Leu Leu
91      1          5          10          15
92 Arg Ala Phe Thr Ile Thr Ala Pro Lys Asp Leu Tyr Val Val Glu Tyr
93      20          25          30
94 Gly Ser Asn Val Thr Met Glu Cys Arg Phe Pro Val Glu Arg Glu Leu
95      35          40          45
96 Asp Leu Leu Ala Leu Val Val Tyr Trp Glu Lys Glu Asp Glu Gln Val
97      50          55          60
98 Ile Gln Phe Val Ala Gly Glu Glu Asp Leu Lys Pro Gln His Ser Asn
99      65          70          75          80
100 Phe Arg Gly Arg Ala Ser Leu Pro Lys Asp Gln Leu Leu Lys Gly Asn
101      85          90          95
102 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
103      100          105          110
104 Cys Cys Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Leu
105      115          120          125
106 Lys Val Asn Ala Pro Tyr Arg Lys Ile Asn Gln Arg Ile Ser Val Asp
107      130          135          140
108 Pro Ala Thr Ser Glu His Glu Leu Ile Cys Gln Ala Glu Gly Tyr Pro
109      145          150          155          160
110 Glu Ala Glu Val Ile Trp Thr Asn Ser Asp His Gln Pro Val Ser Gly

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111                               165                               170                               175
112 Lys Arg Ser Val Thr Thr Ser Arg Thr Glu Gly Met Leu Leu Asn Val
113                               180                               185                               190
114 Thr Ser Ser Leu Arg Val Asn Ala Thr Ala Asn Asp Val Phe Tyr Cys
115                               195                               200                               205
116 Thr Phe Trp Arg Ser Gln Pro Gly Gln Asn His Thr Ala Glu Leu Ile
117                               210                               215                               220
118 Ile Pro Glu Leu Pro Ala Thr His Pro Pro Gln Asn Arg Thr His Trp
119 225                               230                               235                               240
120 Val Leu Leu Gly Ser Ile Leu Leu Phe Leu Ile Val Val Ser Thr Val
121                               245                               250                               255
122 Leu Leu Phe Leu Arg Lys Gln Val Arg Met Leu Asp Val Glu Lys Cys
123                               260                               265                               270
124 Gly Val Glu Asp Thr Ser Ser Lys Asn Arg Asn Asp Thr Gln Phe Glu
125                               275                               280                               285
126 Glu Thr
127                               290
129 <210> SEQ ID NO: 4
130 <211> LENGTH: 873
131 <212> TYPE: DNA
132 <213> ORGANISM: Mus musculus
134 <220> FEATURE:
135 <221> NAME/KEY: CDS
136 <222> LOCATION: (1)...(870)
138 <400> SEQUENCE: 4
139 atg agg ata ttt gct ggc att ata ttc aca gcc tgc tgt cac ttg cta      48
140 Met Arg Ile Phe Ala Gly Ile Ile Phe Thr Ala Cys Cys His Leu Leu
141 1                               5                               10                               15
143 cgg gcg ttt act atc acg gct cca aag gac ttg tac gtg gtg gag tat      96
144 Arg Ala Phe Thr Ile Thr Ala Pro Lys Asp Leu Tyr Val Val Glu Tyr
145                               20                               25                               30
147 ggc agc aac gtc acg atg gag tgc aga ttc cct gta gaa cgg gag ctg      144
148 Gly Ser Asn Val Thr Met Glu Cys Arg Phe Pro Val Glu Arg Glu Leu
149                               35                               40                               45
151 gac ctg ctt gcg tta gtg gtg tac tgg gaa aag gaa gat gag caa gtg      192
152 Asp Leu Leu Ala Leu Val Val Tyr Trp Glu Lys Glu Asp Glu Gln Val
153                               50                               55                               60
155 att cag ttt gtg gca gga gag gag gac ctt aag cct cag cac agc aac      240
156 Ile Gln Phe Val Ala Gly Glu Glu Asp Leu Lys Pro Gln His Ser Asn
157 65                               70                               75                               80
159 ttc agg ggg aga gcc tcg ctg cca aag gac cag ctt ttg aag gga aat      288
160 Phe Arg Gly Arg Ala Ser Leu Pro Lys Asp Gln Leu Leu Lys Gly Asn
161                               85                               90                               95
163 gct gcc ctt cag atc aca gac gtc aag ctg cag gac gca ggc gtt tac      336
164 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
165                               100                               105                               110
167 tgc tgc ata atc agc tac ggt ggt gcg gac tac aag cga atc acg ctg      384
168 Cys Cys Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Leu
169                               115                               120                               125

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171 aaa gtc aat gcc cca tac cgc aaa atc aac cag aga att tcc gtg gat      432
172 Lys Val Asn Ala Pro Tyr Arg Lys Ile Asn Gln Arg Ile Ser Val Asp
173      130      135      140
175 ccc gcc act tet gag cat gaa cta cta tgt cag gcc gag ggt tac cca      460
176 Pro Ala Thr Ser Glu His Glu Leu Ile Cys Gln Ala Glu Gly Tyr Pro
177 145      150      155      160
179 gaa gct gag gta atc tgg aca aac agt gac cac caa ccc gtg agt ggg      528
180 Glu Ala Glu Val Ile Trp Thr Asn Ser Asp His Gln Pro Val Ser Gly
181      165      170      175
183 aag aga agt gtc acc act tcc cgg aca gag ggg atg ctt ctc aat gtg      576
184 Lys Arg Ser Val Thr Thr Ser Arg Thr Glu Gly Met Leu Leu Asn Val
185      180      185      190
187 acc agc agt ctg agg gtc aac gcc aca gcg aat gat gtt ttc tac tgt      624
188 Thr Ser Ser Leu Arg Val Asn Ala Thr Ala Asn Asp Val Phe Tyr Cys
189      195      200      205
191 acg ttt tgg aga tca cag cca ggg caa aac cac aca gcg gag ctg atc      672
192 Thr Phe Trp Arg Ser Gln Pro Gly Gln Asn His Thr Ala Glu Leu Ile
193      210      215      220
195 atc cca gaa ctg cct gca aca cat cct cca cag aac agg act cac tgg      720
196 Ile Pro Glu Leu Pro Ala Thr His Pro Pro Gln Asn Arg Thr His Trp
197 225      230      235      240
199 gtg ctt ctg gga tcc atc ctg ttg ttc ctc att gta gtg tcc acg gtc      768
200 Val Leu Leu Gly Ser Ile Leu Leu Phe Leu Ile Val Val Ser Thr Val
201      245      250      255
203 ctc ctc ttc ttg aga aaa caa gtg aga atg cta gat gtg gag aaa tgt      816
204 Leu Leu Phe Leu Arg Lys Gln Val Arg Met Leu Asp Val Glu Lys Cys
205      260      265      270
207 ggc gtt gaa gat aca agc tca aaa aac cga aat gat aca caa ttc gag      864
208 Gly Val Glu Asp Thr Ser Ser Lys Asn Arg Asn Asp Thr Gln Phe Glu
209      275      280      285
211 gag acg taa      873
212 Glu Thr
213      290
215 <210> SEQ ID NO: 5
216 <211> LENGTH: 3616
217 <212> TYPE: DNA
218 <213> ORGANISM: Homo sapiens
220 <220> FEATURE:
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (73)...(942)
224 <400> SEQUENCE: 5
225 cccacgcgtc cgcagcttcc cgaggtctcc caccagccgc gcttctgtcc gcctgcaggg      60
226 cattccagaa ag atg agg ata ttt gct gtc ttt ata ttc atg acc tac tgg      111
227      Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp
228      1      5      10
230 cat ttg ctg aac gca ttt act gtc acg gtt ccc aag gac cta tat gtg      159
231 His Leu Leu Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val
232      15      20      25
234 gta gag tat ggt agc aat atg aca att gaà tgc aaa ttc cca gta gaa      207

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235 Val Glu Tyr Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu
236 30 35 40 45
238 aaa caa tta gac ctg gct gca cta att gtc tat tgg gaa atg gag gat 255
239 Lys Gln Leu Asp Leu Ala Ala Leu Ile Val Tyr Lys Glu Met Glu Asp
240 50 55 60
242 aag aac att att caa ttt gtg cat gga gag gaa gac ctg aag gtt cag 303
243 Lys Asn Ile Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln
244 65 70 75
246 cat agt agc tac aga cag agg gcc cgg ctg ttg aag gac cag ctc tcc 351
247 His Ser Ser Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser
248 80 85 90
250 ctg gga aat gct gca ctt cag atc aca gat gtg aaa ttg cag gat gca 399
251 Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala
252 95 100 105
254 ggg gtg tac cgc tgc atg atc agc tat ggt ggt gcc gac tac aag cga 447
255 Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg
256 110 115 120 125
258 att act gtg aaa gtc aat gcc cca tac aac aaa atc aac caa aga att 495
259 Ile Thr Val Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile
260 130 135 140
262 ttg gtt gtg gat cca gtc acc tct gaa cat gaa ctg aca tgt cag gct 543
263 Leu Val Val Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala
264 145 150 155
266 gag ggc tac ccc aag gcc gaa gtc atc tgg aca agc agt gac cat caa 591
267 Glu Gly Tyr Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln
268 160 165 170
270 gtc ctg agt ggt aag acc acc acc aat tcc aag aga gag gag aag 639
271 Val Leu Ser Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys
272 175 180 185
274 ctt ttc aat gtg acc agc aca ctg aga atc aac aca aca act aat gag 687
275 Leu Phe Asn Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu
276 190 195 200 205
278 att ttc tac tgc act ttt agg aga tta gat cct gag gaa aac cat aca 735
279 Ile Phe Tyr Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr
280 210 215 220
282 gct gaa ttg gtc atc cca gaa cta cct ctg gca cat cct cca aat gaa 783
283 Ala Glu Leu Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu
284 225 230 235
286 agg act cac ttg gta att ctg gga gcc atc tta tta tgc ctt ggt gta 831
287 Arg Thr His Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val
288 240 245 250
290 gca ctg aca ttc atc ttc cgt tta aga aaa ggg aga atg atg gat gtg 879
291 Ala Leu Thr Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val
292 255 260 265
294 aaa aaa tgt ggc atc caa gat aca aac tca aag aag caa agt gat aca 927
295 Lys Lys Cys Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr
296 270 275 280 285
298 cat ttg gag gag acg taatccagca ttggaacttc tgatcttcaa gcagggattc 982
299 His Leu Glu Glu Thr

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